SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hermeking, Heiko
           Vogelstein, Bert
           Kinzler, Kenneth

(ii) TITLE OF THE INVENTION: 14-3-3 SIGMA ARREST THE CELL
       CYCLE

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:
  (A) ADDRESSEE: Banner & Witcoff
  (B) STREET: 1001 G Street, NW
  (C) CITY: Washington
  (D) STATE: DC
  (E) COUNTRY: USA
  (F) ZIP: 20001

(v) COMPUTER READABLE FORM:
  (A) MEDIUM TYPE: Diskette
  (B) COMPUTER: IBM Compatible
  (C) OPERATING SYSTEM: DOS
  (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
  (A) APPLICATION NUMBER:
  (B) FILING DATE: 18-DEC-1997
  (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
  (A) APPLICATION NUMBER:
  (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:
  (A) NAME: Kagan, Sarah A
  (B) REGISTRATION NUMBER: 32141
  (C) REFERENCE/DOCKET NUMBER: 1107.72886

(ix) TELECOMMUNICATION INFORMATION:
  (A) TELEPHONE: 202-508-9100
  (B) TELEFAX: 202-508-9299
  (C) TELEX:

1

(2) INFORMATION FOR SEQ ID NO:1:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1320 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GAGAGACACA GAGTCCGGCA TTGGTCCCAG GCAGCAGTTA GCCCGCCGCC CGCCTGTGTG     60
TCCCCAGAGC CATGGAGAGA GCCAGTCTGA TCCAGAAGGC CAAGCTGGCA GAGCAGGCCG    120
AACGCTATGA GGACATGGCA GCCTTCATGA AAGGCGCCGT GGAGAAGGGC GAGGAGCTCT    180
CCTGCGAAGA GCGAAACCTG CTCTCAGTAG CCTATAAGAA CGTGGTGGGC GGCCAGAGGG    240
CTGCCTGGAG GGTGCTGTCC AGTATTGAGC AGAAAAGCAA CGAGGAGGGC TCGGAGGAGA    300
AGGGGCCCGA GGTGCGTGAG TACCGGGAGA AGGTGGAGAC TGAGCTCCAG GGCGTGTGCG    360
ACACCGTGCT GGGCCTGCTG GACAGCCACC TCATCAAGGA GGCCGGGGAC GCCGAGAGCC    420
GGGTCTTCTA CCTGAAGATG AAGGGTGACT ACTACCGCTA CCTGGCCGAG GTGGCCACCG    480
GTGACGACAA GAAGCGCATC ATTGACTCAG CCCGGTCAGC CTACCAGGAG GCCATGGACA    540
TCAGCAAGAA GGAGATGCCG CCCACCAACC CCATCCGCCT GGGCCTGGCC CTGAACTTTT    600
CCGTCTTCCA CTACGAGATC GCCAACAGCC CCGAGGAGGC CATCTCTCTG GCCAAGACCA    660
CTTTCGACGA GGCCATGGCT GATCTGCACA CCCTCAGCGA GGACTCCTAC AAAGACAGCA    720
CCCTCATCAT GCAGCTGCTG CGAGACAACC TGACACTGTG GACGGCCGAC AACGCCGGGG    780
AAGAGGGGGG CGAGGCTCCC CAGGAGCCCC AGAGCTGAGT GTTGCCCGCC ACCGCCCCGC    840
CCTGCCCCCT CCAGTCCCCC ACCCTGCCGA GAGGACTAGT ATGGGGTGGG AGGCCCCACC    900
CTTCTCCCCT AGGCGCTGTT CTTGCTCCAA AGGGCTCCGT GGAGAGGGAC TGGCAGAGCT    960
GAGGCCACCT GGGGCTGGGG ATCCCACTCT TCTTGCAGCT GTTGAGCGCA CCTAACCACT   1020
GGTCATGCCC CCACCCCTGC TCTCCGCACC CGCTTCCTCC CGACCCCAGG ACCAGGCTAC   1080
TTCTCCCCTC CTCTTGCCTC CCTCCTGCCC CTGCTGCCTC TGATCGTAGG AATTGAGGAG   1140
TGTCCCGCCT TGTGGCTGAG AACTGGACAG TGGCAGGGGC TGGAGATGGG TGTGTGTGTG   1200
TGTGTGTGTG TGTGTGTGTG CGCGCGCGCC AGTGCAAGAC CGAGACTGAG GGAAAGCATG   1260
TCTGCTGGGT GTGACCATGT TTCCTCTCAA TAAAGTTCCC CTGTGACACT CAAAAAAAAA   1320
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    (2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 248 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Glu Arg Ala Ser Leu Ile Gln Lys Ala Lys Leu Ala Glu Gln Ala
1               5                   10                  15
Glu Arg Tyr Glu Asp Met Ala Ala Phe Met Lys Gly Ala Val Glu Lys
            20                  25                  30
Gly Glu Glu Leu Ser Cys Glu Glu Arg Asn Leu Leu Ser Val Ala Tyr
            35                  40                  45
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2

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Lys Asn Val Val Gly Gly Gln Arg Ala Ala Trp Arg Val Leu Ser Ser
    50                  55                  60
Ile Glu Gln Lys Ser Asn Glu Glu Gly Ser Glu Glu Lys Gly Pro Glu
65                  70                  75                  80
Val Arg Glu Tyr Arg Glu Lys Val Glu Thr Glu Leu Gln Gly Val Cys
                85                  90                  95
Asp Thr Val Leu Gly Leu Leu Asp Ser His Leu Ile Lys Glu Ala Gly
            100                 105                 110
Asp Ala Glu Ser Arg Val Phe Tyr Leu Lys Met Lys Gly Asp Tyr Tyr
            115                 120                 125
Arg Tyr Leu Ala Glu Val Ala Thr Gly Asp Asp Lys Lys Arg Ile Ile
        130                 135                 140
Asp Ser Ala Arg Ser Ala Tyr Gln Glu Ala Met Asp Ile Ser Lys Lys
145                 150                 155                 160
Glu Met Pro Pro Thr Asn Pro Ile Arg Leu Gly Leu Ala Leu Asn Phe
                165                 170                 175
Ser Val Phe His Tyr Glu Ile Ala Asn Ser Pro Glu Glu Ala Ile Ser
            180                 185                 190
Leu Ala Lys Thr Thr Phe Asp Glu Ala Met Ala Asp Leu His Thr Leu
            195                 200                 205
Ser Glu Asp Ser Tyr Lys Asp Ser Thr Leu Ile Met Gln Leu Leu Arg
    210                 215                 220
Asp Asn Leu Thr Leu Trp Thr Ala Asp Asn Ala Gly Glu Glu Gly Gly
225                 230                 235                 240
Glu Ala Pro Gln Glu Pro Gln Ser
                245
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        (2) INFORMATION FOR SEQ ID NO:3:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 7680 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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GGATCCCAGC CTGCCCCTCC ACTTCTCTCC CAAGCCAGGT CCCGGCATGG GTGGGTTATG    60
CTCATGCTGG CAATACTTGA AACGGGTTTA TTAATGCTGG GTATTTTGCA CAATTTTATA   120
GACCTCTTTT CTACATAGTC TTTTTTAAAT GGAAGGAGAA AATGTCAGCC ACATTACTGT   180
CTGTGTAGTG CCAGGTGAAG GGTTATCAGA AGGCTGGTTG GTTTTAATAA GTTTATTCCA   240
AGAGACCTTC TGGCTGGAAT GAGTGAGAGT GTGTGTGCAT GTGTGTGTGT GTTCATGTGT   300
GCCCTGTATG AATGTGGCTG GCTCCCAGAT CCCCTGGGCT GCCCCCTGCC CCATCCCCTT   360
TGAGTATCAG AAGCACTCTG AGCCAAGGGG ACAGGGGGCA CGTGCACTGG TCACGAGAAA   420
ACCCTGGGCT CCCACTGGGG CTCAGCCCAG CCTCCTATCT TTCCTTCTTC TATGGACTTC   480
AGACAGCCAG TGTCTGGGGA CTCTGCCACT CTACCCCCAG CCCTACCCAC CAGCCCCCAG   540
GTGAGGCTTC CAGCTGGGAC CTGCCCAGAC AGGCTGAGCC TGGGCGTGGT GGGTGGGGTG   600
ATGGCTCTGG GGAGCGGCTG CCATCCTACA AGCCACACCC CCTCCTCTGA GCTCTGAATA   660
TGGGACCCAG TGCCAGGAGC TGGAAGACAA GGTGTTTCTG CCAAACGGGA CCTCCATCCA   720
GAGAAAAGGA AGAAGGTGCA GGGTGGGCCA AGAGGCAAGT GAAGGTTGGC CTGAGTCTGG   780
GCCGGAAACT CAGAGGATGT TTCTCCTCTG CTGGGAGCTG TAGTTTCTTA TCAAAATAGA   840
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3

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TATTGTTCCA CCATCCCCCT CCTTGGCCCT TCAAGTGGGC TGAAGCCTTG GAAAGTGACA    900
TAGGAAGTCC CCAGATCTTG CCCTTCTCAC TCCAGAGGCT AGTGGTCACA GACAGCTGGG    960
AATGGCAGCC ACAGAGGGTC CCTCTGGAGA AACAGCTTCA CCCCAGCCTC AGGGCCCTGG   1020
GCATCACTGC AGTGGCCCTG GGAGGTGAGG AAGAAGCTGG CTAGAGGAGG GGGCTCCCAC   1080
CTACCTTTTA TTTAAGCCAG TATTCTTTGT TCCTGCTTGT AATAAAACTT CAGTTTATAA   1140
GAGTTGCTTT GCTTTGGTTT GGTTTTTGTT TGCTTTTCCT TTGCTGAGGC CCCAACTGGG   1200
AGCCCTCTGT TCTTTCAGAC AAATTTGGTT CTTTCCTGGG GAGACTGTGA GAAGGCAGGC   1260
AGCCCAGTGA TCTGGCTACA TTTTCCCTCA CCTGGCTGGA GCTCTGTCCG CTGGAGGAAG   1320
AGCAGAGAGG GCTGCGGCTG AGCCCCCATG GGCACGTGAA AAGAGGCCAT CCTGTCCCCT   1380
CTTTGTCCCC TCCACCTTCC CCTGCCTCAG GGGCTTGGAG ACCCCAAATT CTTCTTCCCT   1440
ACTGCCTTTC CACTCCGATC CCCAATGAGT GCCCAGCTAA GAAAATGTTT GAGACAGTAG   1500
ATTCCAGTTT GAGAGCCGGA GCTTCCCTGG CTACCACCTC CAACCTGGGC ACCAGGGCCC   1560
AGCCAGACAA CTCATAACAC TGGCCCACCT CTCTGGTATC TCCCTCAGGA GGACACCTGT   1620
CAGGATTTTG CCATCTCCTG CACAGCCTGA GGGGAGCTAA CAGGCCTCTT TGCAGAGGGT   1680
TAGCTGGTAA GACCGTTTCT TCCCTGTCGG CCAGCACTGC CCGCTCCCCT CCACACACCA   1740
TCTCATCCTC ATCGCATGCC TCGCCAACCC CATGGAGCCC GTCCATCTGT CTGGTGTGTG   1800
GTGCGGTGTG TGTGCTGGTG GTGGTAGGGT CTCCAGGGAC TCCCCGCTAA GCAGAAGGAT   1860
CGGGATATAG GGCAAGGCTA AAAGCCCAGC CCCATTGTGG ACTGAGGAAG TACGTTCGCG   1920
CAGAGCAGCT CTCCAGCTGG AAGAGGAGGT GGAGGGTGAG GCTGGGGAGA GGATGGCGAA   1980
CCTGCCCTGA GGTGCTTGGG TCTGTGCTGG TGGGGTCCTG GTATGCAGGG GCCACCGGTC   2040
ACTAACACTC TTATGTCCTG GCTTTCTGTC CCCGCTGAGC TTTCTCTCAC CCGCCCGTTT   2100
TCTCTCCTGC TTCATTGCCT GCTGCCTAAG CCTTGGCCCT TCTCTCGGGC AGAGGCAGGT   2160
GCTGTGGCAG CACCTCTCCC CACCACCGGG CCCCTGCAGG CCGCCTCCCT CCTCCCAGGC   2220
CTGCTAACCC TCTCTCTTCT CCTTCTTTGC TGTCCTGCCG GGGATCTCCA GTGTGTGCGG   2280
GGGCTTAAGG ACCTCCTGAG GACCGCTGCT CTCTGCCTCT CCAGGAATGG CCTGGGGGGA   2340
GCCAGGCACC CGGCACCTCC ACCTGCCTAA CCTGTGGCCC ATCTGCCACC ATCTGTGCCT   2400
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GGGCTGGCCT CTTTGCCCCA TTCCCGCTCC ATGCCGGCCA GAGTGTAGAA AGCCATAACG   2520
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GACTTCCCCT TCCCGGATTT GTGAGGTGTC AAGACTAGGA ATCTGGCCTT AGAGCCTGCC   2640
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GCTGAGCCCA GGGCTGGGGG CTGCTTGTCT GCTATCCTGT ACCTTTTTTT TTTTAACCA   3000
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ACAGAGGGTT TAACTCCAGT TTGGGACTGC CATACCCATG AACTGAGCCC AGCCCAGGGT   3360
AACGATCTCA TGGAAACTTC TCTCTCCCCA GTTGCTGCAC TACATCAAGA TACACACATG   3420
TGCATACACT GTACTATGGG CTAAAAAAAT ACGTACCGCT ACCGTTCAGC AAGGGCTTGC   3480
CGAGTCCCGG GCCCATTTTC TCATCTTAAC CTGTGAGGAG GATGATGTCA GCCTTTTTAC   3540
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GAGAAATTGA AGCCCAGAGG CAGGAAGGGA CCTGCCCAAG GCCTTATAAC AGAGCTGGGA   3840
TGCAGTCCCA CACTCTGACC TCATTCCATT CTCTCTCCAT AAATTCTGCA CTGTCTCTAG   3900
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4

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AGAACTACGA ATCACTTAAA AGTAATGTAA GCTACTCTGG GCACACTGCC TATGGGGTCG    4020
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AAAAGGTGCT AGAGCTTCCT CTGGCCACCT GTTTAATTTG ATCATTCCAA GACAGAAACA    4200
TTTCTTAGGA AGTTCTTTCT AGAATCTACC TGGTGTCCCT CCCACTGCTA TCAGAGCCCT    4260
GTCCTCTGTC CTCAGTGGAG GTAGAGAGCA AATGGTTGCT GCTTTCTTCA TCACAACCCT    4320
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CTGCTGGTAG AATGGATGCT GTACAGGAGG GTGGGGAGGT AGCAGGCAGA ATGAGGAAAG    4440
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GCGGGCAGGA GGTATCAGGC AGCCTGGCTC CCAGATGCAC CCCTGAGCTC CAGCAGGGGA    4680
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CCACCAGGTC CTCTGGCTTA AGTGGCGGGA AGCAAATGGT CCCTCCCTGG ACTCAGGCTC    4800
CAAAGTTCCT GGGCCTGCCT TCCAGGTTCC CAGTGTCCTG GGATCTCCAG CTTTCCCCAG    4860
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TGCCTCAGCC TCCCGAGTAG CTGGGACTAC AGGCATGTGC CACCATGCCC GGCTAATTTT    6120
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TGAAATTATC CTGGCTCAAC TATTAGGTCG GCAGAATCCC AGTGAAGGGA GCCCTACCTC    6960
TGAGCCCCAT CTAAGCTTTG GCTATGGGTG GGGCAGATAA GCAGGAATCC ATCCCTATAG    7020
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5

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AGCAGGGAAA GAACGTTGGC AACAGAGGTC TCCATCTCTG AGGACTCTGC CAGGGGTCAG      7140
AGATGGGGCA ATGGTCAAAA GGAAGGAACA GGCCAGGCAC AGTGGCTCAT GCCCATAATC      7200
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TGGGCAATGT AGTGAGATCT GCTCTCTATT TAAAAAAAAA AAAAAGGAAA GAACAAGTAA      7320
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GAATGGTATG TGTCACTGCC ACCTCCCTTT CTCAGTCCTC TCTCTCCCCA GGTTGCTAGC      7440
GTCCCCCTGG GGGATCAAAC TGGACTGCTT CCCAGCCTCA GACAGAGAGC AGTCTGAGTC      7500
AGGCAGGAAA GTGGGACAGC CGGGGAGCTG GACCCCACCC TCTGTGAGCC CCGCTGGTAC      7560
CTGATGGCAT GTGGCTTGGA GAGGGCAGGT GACCTGGCGT GGAGGGCCAG AGGGTAAATC      7620
CTCAAACAAG TGGCAACAGG CCACCAACTT GAAAGGGAAA ATTGTGTAGT GATGGGAAAT      7680
```

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 20 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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AGGCATGTGC CACCATGCCC                                                    20
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(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 23 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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GTAGCATTAG CCCAGACATG TCC                                                23
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